

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wong, Hing C.  
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- (ii) TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 123
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Dade International, Inc.
  - (B) STREET: 1717 Deerfield Road
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  - (E) COUNTRY: USA
  - (F) ZIP: 60015
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
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- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/283,302
  - (B) FILING DATE: 29-JUL-1994
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

09843154-050301

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 1                      5                      10

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCACCATG

8

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala  
 1                      5                      10                      15  
 Gly Arg

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ile Ser Gln Ala Val His Ala Ala Arg Ala Glu Ile Asn Glu Ala  
 1                      5                      10                      15  
 Gly Arg

(2) INFORMATION FOR SEQ ID NO:5:

00843164-050301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Arg

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

Asn Leu Cys Asn Ile Pro Cys Ser Ala Leu Leu Ser Ser  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

Gln Ile Ser Val Gln Pro Ala Phe Ser Val Gln  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
GATGATATCA GAGAGAAATA CATACTAACA CAC

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
CGGAAGAAAG AGACTTCGGC CGCTACTTAC

30

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
GTGTGTTAGT ATGTATTTCT CTCTGATATC TTCAGCTTCC AGCAGTG

47

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
TCTTCTAGAA GACCACGCTA C

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
GATGATATCC GGCCGAAGTC TCTTTCTTCC GTTGTC

36

(2) INFORMATION FOR SEQ ID NO:18:

00040154-050301  
T0E0S0-49T0H060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGTCTCCTC AGGTACGGCC GGCCTCTCCA GGTCTTCG

38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CACAGTTATC CACTCTGTCT TTGATATCAC AGGTGTCCT

39

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

1

5

10

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(B) 101-345017-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

3

5

10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(B) 101-325017-111111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

1

15

Arg

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(B) 10-000000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

1

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGGGGGGCCA TGGCCGAAGA CGACATTGAG GCCGAC

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGGCGACTA GTCCAGTGTT TCAGAACCGG CTC

33

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCCCGATA TCTCAGCTTC CAGCAGTGGA GACGACATTG AG

42

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCCCCC GGC CGCTACTTAC GTTCCAGTG TTTCAGAACC GG

42

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGGGGCCA TGGCCGAAA CTCCGAAAGG CATTTTCG

37

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

39

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCCGATA TCACAGGTGT CTTAAGTGCT AGCGGAGGGG GCGGAAGCGG CGGAGGGGGA

60

AACTCCGAAA GGCATTTC

78

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGCTTGATAT CACAGGTGTC TTAAGTGGAG

30

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTAGCTCCAC TTAAGACACC TGTGATATCA

30

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TCCGGAGGCG GCGGAGACTC CGAAAGGCAT TTCG

34

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGATCGCTAG CGGCGGTGGT GGTTCGGTG GCGGCGGAG

39

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCCCCAGGC TTCCCGGGCC ACCATGCCGT GCAGCAGAGC TC

42

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCCCCGAGC TCGAATTCTC ATAAAGGCCC TGGGTGTCTG

40

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown

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(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCCCAAGC TTCCCGGGCC ACCATGGCTC TGCAGATCCC CAGC

44

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCCCACTT AAGGTCCTTG GGCTGCTCAG CACC

34

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCCCCCCCAT CACTGTGGAG TGGAGGG

27

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCCGAGC TCGAATTCTC ACTGCAGGAG CCCTGCTGG

39

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGGGAAGC TTATGATCAA AGAAGACAT GTGATCATC

39

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## 36

## 46

## 39

## 36

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGGGGGAAGC TTGATATCTC AGCTTCCAGC AGTAGTATCA AAGAAGAACA TGTGATC

57

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGGGGCGGC CGCTACTTAC GTTTCTCTGG GAGAGGGCTT GGAGC

45

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GCGGCGGGAT CCCTTGCTCT GTGCAGATTC AGACC

35

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGGGGGGCCA TGGCCGATC CGCTAGCGGG GACACCCGAC CACGTTTCTT G

51

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCGGCGACTA GTCTTGCTCT GTGCAGATTC AGACCG

36

(2) INFORMATION FOR SEQ ID NO:54:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTGTCTTAA GTGGAGCTAG CGGAGGGGGC GGGTCCGGAG GTGGTGGGGA CACCCG

56

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GAAATGACAT TCAAACCTCA GCTGCCACAA GAAACGTGGT CGGGTGTCCT CACCACC

57

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGGGCGGC CGTACCTGAG GACTTGCTCT GTGCAGATTC AG

42

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTAAGTATCT CTCAGGCTGT TCACGCTGCT CACGCTGAAA TCAACGAAGC TGGTCGTG

58

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

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CTAGCACGAC CAGCTTCGTT GATTTTCAGCC TGAGCAGCGT GAACAGCCTG AGAGATAC 58

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTAAGTATCT CTCAGGCTGT TCACGCTGCT CGGGCTGAAA TCAACGAAGC TGGTCGTG 58

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTAGCACGAC CAGCTTCGTT GATTTTCAGCC CGAGCAGCGT GAACAGCCTG AGAGATAC 58

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TTAAGTATCT CTCAGGCTGT TCACGCTGCT CACTACGAAA TCAACGAAGC TGGTCGTG 58

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTAGCACGAC CAGCTTCGTT GATTTTCATAG TGAGCAGCGT GAACAGCCTG AGAGATAC 58

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

46

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

46

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

40

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

40

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

46



(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTAGCGGTGG CCAGCTTCAG GGTGTTCTGC TTCACGTACT TGGGAC

46

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TTAAGTCACT ATGGCTCCCT GCCGCAGAAG TCCCAGCACG GGCGCG

46

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTAGCGCGCC CGTGCTGGGA CTTCTGCGGC AGGGAGCCAT AGTGAC

46

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTACATCACT CCCTGGGCAA GTGGCTGGGC CACCCGGACA AGTTCCG

46

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown

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49.

49

45

46

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Ser Ser Glu Asp Asp Ile Glu Ala Asp His  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Val Leu Lys His Trp Lys Arg  
 1 5

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GATATCACAG GTGTCTTAAG TGGAGCTAGC GGAGGGGGCG GAAGCGGCGG AGGGGGAAAC 60  
 .TCCGAAAGGC AT 72

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATCACTGTGG AGTGGTCCTC AGGTACGGCC GCC 33

(2) INFORMATION FOR SEQ ID NO:81:

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SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

Val Leu Ser Gly Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn  
1 5 10 15

Ser Glu Arg His  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids -  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

Ile Thr Val Glu Trp Ser Ser  
1 5

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS
- (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

GATATCTCAG CTTCCAGCAG TGAAGACGAC ATTGAGGCCG ACCAC

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

CCGGTTCTGA AACACTGGAA ACGTAAGTAG CGGCCG

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Ser Ser Ser Glu Asp Asp Ile Glu Ala Asp His  
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Pro Val Leu Lys His Trp Lys Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATATCACAG GTGTCTTAAG TGGAGCTAGC GGCGGTGGTG GTTCCGGTGG CGGCGGAGAC  
TCCGAAAGGC AT

60

72

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATCACTGTGG AGTGGTCCTC AGGTACGGCC GCC

33

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Val Leu Ser Gly Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asp  
 1 5 10 15  
 Ser Glu Arg His  
 20

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ile Thr Val Glu Trp Ser Ser  
 1 5

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GATATCTCAG CTTCCAGCAG TATCAAAGAA GAACATGTGA TCATC

45

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CCAGAGACTA CAGAGAACAA ACGTAAGTAG CGGCCG

36

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

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Ser Ser Ser Ile Lys Glu Glu His Val Ile Ile  
1 5 10

(2) INFORMATION FOR SEQ ID. NO:94:

(i) SEQUENCE CHARACTERISTICS:  
 1. LENGTH: 8 amino acid

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Pro Glu Thr Thr Glu Asn Lys Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

(xi) SEQUENCE DESCRIPTION

GATATCACAG GTGTCTTAAG TGGAGCTAGC GGAGGGGGCG GGTTCCGAGG TGGTGGGGAC	60
ACCCGACCAC GTTTCCTTGTG GCAGCTGAAG	90

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pair

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCTGAATCTG CACAGAGCAA GTCCTCAGGT ACGGCCG

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS: 26 amino acids

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

(xi) SEQUENCE DESCRIPTION

Val Leu Ser Gly Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asp  
1 5 10 15

Thr Arg Pro Arg Phe Leu Trp Gln Leu Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser Glu Ser Ala Gln Ser Lys Ser Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTCCAGCTGT CTTGTTTCAG TACTGATC

28

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTAAGTAGCG GCCG

14

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGTATGTAAA AATAACATC ACAG

24

(2) INFORMATION FOR SEQ ID NO:102:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCTTTGCTTA CGGAGTTACT C

21

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 95 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCCCGGCCAC CATGCCGTGC AGCAGAGCTC TGATTCTGGG GGTCCTCGCC CTGAACACCA

60

TGCTCAGCCT CTGCGGAGGT GAAGACGACA TTGAG

95

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGATCAGGTG GCACCTCCAG ACACCCAGGG CCTTTATGAG AATTC

45

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr  
 1 5 10 15

Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu  
 20 25

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Arg Ser Gly Gly Thr Ser Arg His Pro Gly Pro Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 194 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

AAGCTTCCCG GGCCACCATG GCTCTGCAGA TCCCAGCCT CCTCCTCTCA GCTGCTGTGG 60  
 TGGTGCTGAT GGTGCTGAGC AGCCCAAGGA CCTTAAGTAT CTCTCAGGCT GTTCACGCTG 120  
 CTCACGCTGA AATCAACGAA GCTGGTCGTG CTAGCGGAGG GGGCGGAAGC GGCGGAGGGG 180  
 GAAACTCCGA AAGG 194

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CCTCCTCCAG CAGGGCTCCT GCAGTGAGAA TTCGAGCTC 39

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val  
 1 5 10 15  
 Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln Ala Val  
 20 25 30

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His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser Gly Gly  
35 40 45

Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg  
50 55

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Pro Pro Pro Ala Gly Leu Leu Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CCCCCCCCGC GGCCGCCCCA CCATGGGACT GAGTAACATT CTC

43

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCCCCGCGG CCGCTTTAAA AACATGTATC ACTTTT

36

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCCGCCA TGGCCGCTAG CGGAGGGGGC GGAAGC

36

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CCCGGGGCCT CGAGTGAAGA CGACATTGAG GCCGAC

36

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CCCCCACTA GTCCACTCCA CAGTGATGGG GCT

33

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CCCCCCCCCG GGACCAAGTGT TTCAGAACCG GCTCCTC

37

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 65 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

TCGAGGAACC GCCACCGCCA GAACCGCCGC CACCGGAACC ACCACCGCCG CTGCCACCGC

60

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

60

65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 6..1382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG	47
Met Ala Leu Gln Ile Pro Ser Leu Leu Ser Ala Ala Val	
1 5 10	
GTG GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG	95
Val Val Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln	
15 20 25 30	
GCT GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC	143
Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser	
35 40 45	
GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG	191
Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg His Phe Val	
50 55 60	
GTC CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA	239
Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile	
65 70 75	
CGG CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC	287
Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr	
80 85 90	
GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA	335
Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro	
95 100 105 110	
GAC GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG	383
Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg	
115 120 125	
GCC GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC	431
Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr Glu Gly Pro Glu Thr	
130 135 140	
AGC ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG	479
Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu	
145 150 155	
TCC AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG	527
Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser Val	
160 165 170	
ACA GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC	575
Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly	
175 180 185 190	
CAG GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG	623
Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly	
195 200 205	
GAC TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG	671

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Asp	Trp	Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	
			210					215					220			
GGA	GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	CCC	719
Gly	Glu	Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	
		225					230					235				
ATC	ACT	GTG	GAG	TGG	ACT	AGT	GGT	GGC	GGT	GGC	AGC	GGC	GGT	GGT	GGT	767
Ile	Thr	Val	Glu	Trp	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
	240					245					250					
TCC	GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCG	AGT	GAA	GAC	GAC	815
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Glu	Asp	Asp	
	255				260					265					270	
ATT	GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	863
Ile	Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	
				275					280					285		
CCT	GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	GAT	GAG	TTG	911
Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Leu	
			290					295					300			
TTC	TAT	GTG	GAC	TTG	GAT	AAG	AAG	AAA	ACT	GTC	TGG	AGG	CTT	CCT	GAG	959
Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr	Val	Trp	Arg	Leu	Pro	Glu	
		305					310					315				
TTT	GGC	CAA	TTG	ATA	CTC	TTT	GAG	CCC	CAA	GGT	GGA	CTG	CAA	AAC	ATA	1007
Phe	Gly	Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	
	320					325					330					
GCT	GCA	GAA	AAA	CAC	AAC	TTG	GGA	ATC	TTG	ACT	AAG	AGG	TCA	AAT	TTC	1055
Ala	Ala	Glu	Lys	His	Asn	Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Phe	
	335				340					345					350	
ACC	CCA	GCT	ACC	AAT	GAG	GCT	CCT	CAA	GCG	ACT	GTG	TTC	CCC	AAG	TCC	1103
Thr	Pro	Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	
				355					360					365		
CCT	GTG	CTG	CTG	GGT	CAG	CCC	AAC	ACC	CTT	ATC	TGC	TTT	GTG	GAC	AAC	1151
Pro	Val	Leu	Leu	Gly	Gln	Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	
			370				375						380			
ATC	TTC	CCA	CCT	GTG	ATC	AAC	ATC	ACA	TGG	CTC	AGA	AAT	AGC	AAG	TCA	1199
Ile	Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	
		385					390					395				
GTC	ACA	GAC	GGC	GTT	TAT	GAG	ACC	AGC	TTC	CTC	GTC	AAC	CGT	GAC	CAT	1247
Val	Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	
	400					405					410					
TCC	TTC	CAC	AAG	CTG	TCT	TAT	CTC	ACC	TTC	ATC	CCT	TCT	GAT	GAT	GAC	1295
Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	
	415				420					425					430	
ATT	TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC	CTG	GAG	GAG	CCG	GTT	CTG	1343
Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	
				435					440					445		

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AAA CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG 1385  
Lys His Trp Ser Arg Ala Ser His His His His His  
450 455

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1508 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 6..1505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG 47  
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val  
460 465 470

GTG GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG 95  
Val Val Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln  
475 480 485

GCT GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC 143  
Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser  
490 495 500 505

GGA GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG 191  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg His Phe Val  
510 515 520

GTC CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA 239  
Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile  
525 530 535

CGG CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC 287  
Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr  
540 545 550

GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA 335  
Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro  
555 560 565

GAC GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG 383  
Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg  
570 575 580 585

GCC GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC 431  
Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr Glu Gly Pro Glu Thr  
590 595 600

AGC ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG 479  
Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu

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605						610						615						
TCC Ser	AGG Arg	ACA Thr 620	GAG Glu	GCC Ala	CTC Leu	AAC Asn	CAC His 625	CAC His	AAC Asn	ACT Thr	CTG Leu	GTC Val 630	TGT Cys	TCG Ser	GTG Val	527		
ACA Thr	GAT Asp 635	TTC Phe	TAC Tyr	CCA Pro	GCC Ala	AAG Lys 640	ATC Ile	AAA Lys	GTG Val	CGC Arg	TGG Trp 645	TTC Phe	AGG Arg	AAT Asn	GGC Gly	575		
CAG Gln 650	GAG Glu	GAG Glu	ACA Thr	GTG Val	GGG Gly 655	GTC Val	TCA Ser	TCC Ser	ACA Thr	CAG Gln 660	CTT Leu	ATT Ile	AGG Arg	AAT Asn	GGG Gly 665	623		
GAC Asp	TGG Trp	ACC Thr	TTC Phe	CAG Gln 670	GTC Val	CTG Leu	GTC Val	ATG Met	CTG Leu 675	GAG Glu	ATG Met	ACC Thr	CCT Pro	CAT His 680	CAG Gln	671		
GGA Gly	GAG Glu	GTC Val	TAC Tyr 685	ACC Thr	TGC Cys	CAT His	GTG Val	GAG Glu 690	CAT His	CCC Pro	AGC Ser	CTG Leu	AAG Lys 695	AGC Ser	CCC Pro	719		
ATC Ile	ACT Thr	GTG Val 700	GAG Glu	TGG Trp	ACT Thr	AGT Ser	GGT Gly 705	GGC Gly	GGT Gly	GGC Gly	AGC Ser	GGC Gly 710	GGT Gly	GGT Gly	GGT Gly	767		
TCC Ser	GGT Gly 715	GGC Gly	GGC Gly	GGT Gly	TCT Ser	GGC Gly 720	GGT Gly	GGC Gly	GGT Gly	TCC Ser	TCG Ser 725	AGT Ser	GAA Glu	GAC Asp	GAC Asp	815		
ATT Ile 730	GAG Glu	GCC Ala	GAC Asp	CAC His	GTA Val 735	GGC Gly	TTC Phe	TAT Tyr	GGT Gly	ACA Thr 740	ACT Thr	GTT Val	TAT Tyr	CAG Gln	TCT Ser 745	863		
CCT Pro	GGA Gly	GAC Asp	ATT Ile	GGC Gly 750	CAG Gln	TAC Tyr	ACA Thr	CAT His	GAA Glu 755	TTT Phe	GAT Asp	GGT Gly	GAT Asp	GAG Glu 760	TTG Leu	911		
TTC Phe	TAT Tyr	GTG Val	GAC Asp 765	TTG Leu	GAT Asp	AAG Lys	AAG Lys	AAA Lys 770	ACT Thr	GTC Val	TGG Trp	AGG Arg	CTT Leu 775	CCT Pro	GAG Glu	959		
TTT Phe	GGC Gly	CAA Gln 780	TTG Leu	ATA Ile	CTC Leu	TTT Phe	GAG Glu 785	CCC Pro	CAA Gln	GGT Gly	GGA Gly	CTG Leu 790	CAA Gln	AAC Asn	ATA Ile	1007		
GCT Ala	GCA Ala 795	GAA Glu	AAA Lys	CAC His	AAC Asn	TTG Leu 800	GGA Gly	ATC Ile	TTG Leu	ACT Thr	AAG Lys 805	AGG Arg	TCA Ser	AAT Asn	TTC Phe	1055		
ACC Thr 810	CCA Pro	GCT Ala	ACC Thr	AAT Asn	GAG Glu 815	GCT Ala	CCT Pro	CAA Gln	GCG Ala	ACT Thr 820	GTG Val	TTC Phe	CCC Pro	AAG Lys	TCC Ser 825	1103		
CCT Pro	GTG Val	CTG Leu	CTG Leu	GGT Gly 830	CAG Gln	CCC Pro	AAC Asn	ACC Thr	CTT Leu 835	ATC Ile	TGC Cys	TTT Phe	GTG Val	GAC Asp 840	AAC Asn	1151		
ATC	TTC	CCA	CCT	GTG	ATC	AAC	ATC	ACA	TGG	CTC	AGA	AAT	AGC	AAG	TCA	1199		

Ile	Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser		
			845					850					855				
GTC	ACA	GAC	GGC	GTT	TAT	GAG	ACC	AGC	TTC	CTC	GTC	AAC	CGT	GAC	CAT	1247	
Val	Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His		
		860					865					870					
TCC	TTC	CAC	AAG	CTG	TCT	TAT	CTC	ACC	TTC	ATC	CCT	TCT	GAT	GAT	GAC	1295	
Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp		
		875				880					885						
ATT	TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC	CTG	GAG	GAG	CCG	GTT	CTG	1343	
Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu		
		890				895				900					905		
AAA	CAC	TGG	GAA	CCT	GAG	ATT	CCA	GCC	CCC	ATG	TCA	GAG	CTG	ACA	GAA	1391	
Lys	His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu		
				910					915					920			
ACT	GTG	GTG	TGT	GCC	CTG	GGG	TTG	TCT	GTG	GGC	CTT	GTG	GGC	ATC	GTG	1439	
Thr	Val	Val	Cys	Ala	Leu	Gly	Leu	Ser	Val	Gly	Leu	Val	Gly	Ile	Val		
			925					930					935				
GTG	GGC	ACC	ATC	TTC	ATC	ATT	CAA	GGC	CTG	CGA	TCA	GGT	GGC	ACC	TCC	1487	
Val	Gly	Thr	Ile	Phe	Ile	Ile	Gln	Gly	Leu	Arg	Ser	Gly	Gly	Thr	Ser		
		940					945					950					
AGA	CAC	CCA	GGG	CCT	TTA	TGA										1508	
Arg	His	Pro	Gly	Pro	Leu												
			955														

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 6..1382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CCACC	ATG	GCT	CTG	CAG	ATC	CCC	AGC	CTC	CTC	CTC	TCA	GCT	GCT	GTG		47
Met	Ala	Leu	Gln	Ile	Pro	Ser	Leu	Leu	Leu	Ser	Ala	Ala	Val			
					505					510						
GTG	GTG	CTG	ATG	GTG	CTG	AGC	AGC	CCA	AGG	ACC	TTA	AGT	ATC	TCT	CAG	95
Val	Val	Leu	Met	Val	Leu	Ser	Ser	Pro	Arg	Thr	Leu	Ser	Ile	Ser	Gln	
		515			520					525					530	
GCT	GTT	CAC	GCT	GCT	CAC	GCT	GAA	ATC	AAC	GAA	GCT	GGT	CGT	GCT	AGC	143
Ala	Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly	Arg	Ala	Ser	
				535					540					545		

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GGA	GGG	GGC	GGA	AGC	GGC	GGA	GGG	GGA	AAC	TCC	GAA	AGG	CAT	TTC	GTG	191
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Asn	Ser	Glu	Arg	His	Phe	Val	
			550					555					560			
GTC	CAG	TTC	AAG	GGC	GAG	TGC	TAC	TAC	ACC	AAC	GGG	ACG	CAG	CGC	ATA	239
Val	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Tyr	Thr	Asn	Gly	Thr	Gln	Arg	Ile	
		565					570					575				
CGG	CTC	GTG	ACC	AGA	TAC	ATC	TAC	AAC	CGG	GAG	GAG	TAC	GTG	CGC	TAC	287
Arg	Leu	Val	Thr	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Val	Arg	Tyr	
	580					585					590					
GAC	AGC	GAC	GTG	GGC	GAG	TAC	CGC	GCG	GTG	ACC	GAG	CTG	GGG	CGG	CCA	335
Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	Pro	
595					600					605					610	
GAC	GCC	GAG	TAC	TGG	AAC	AGC	CAG	CCG	GAG	ATC	CTG	GAG	CGA	ACG	CGG	383
Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Pro	Glu	Ile	Leu	Glu	Arg	Thr	Arg	
				615					620					625		
GCC	GAG	GTG	GAC	ACG	GCG	TGC	AGA	CAC	AAC	TAC	GAG	GGG	CCG	GAG	ACC	431
Ala	Glu	Val	Asp	Thr	Ala	Cys	Arg	His	Asn	Tyr	Glu	Gly	Pro	Glu	Thr	
			630					635					640			
AGC	ACC	TCC	CTG	CGG	CGG	CTT	GAA	CAG	CCC	AAT	GTC	GCC	ATC	TCC	CTG	479
Ser	Thr	Ser	Leu	Arg	Arg	Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	Leu	
		645					650					655				
TCC	AGG	ACA	GAG	GCC	CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGT	TCG	GTG	527
Ser	Arg	Thr	Glu	Ala	Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	
	660					665					670					
ACA	GAT	TTC	TAC	CCA	GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	AGG	AAT	GGC	575
Thr	Asp	Phe	Tyr	Pro	Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	
675					680				685						690	
CAG	GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	623
Gln	Glu	Glu	Thr	Val	Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	
				695					700					705		
GAC	TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	CAG	671
Asp	Trp	Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	
			710					715					720			
GGA	GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	CCC	719
Gly	Glu	Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	
		725					730					735				
ATC	ACT	GTG	GAG	TGG	ACT	AGT	GGT	GGC	GGT	GGC	AGC	GGC	GGT	GGT	GGT	767
Ile	Thr	Val	Glu	Trp	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
		740				745					750					
TCC	GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCG	AGT	GAA	GAC	GAC	815
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Glu	Asp	Asp	
755					760					765					770	
ATT	GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	863
Ile	Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	
				775					780					785		

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CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG	911
Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu	
790 795 800	
TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG	959
Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu	
805 810 815	
TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA	1007
Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile	
820 825 830	
GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC	1055
Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe	
835 840 845 850	
ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC	1103
Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser	
855 860 865	
CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC	1151
Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn	
870 875 880	
ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA	1199
Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser	
885 890 895	
GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT	1247
Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His	
900 905 910	
TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC	1295
Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp	
915 920 925 930	
ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG	1343
Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu	
935 940 945	
AAA CAC TGG GAG GAA GAA GAG TAC ATG CCG ATG GAA TGA	1382
Lys His Trp Glu Glu Glu Glu Tyr Met Pro Met Glu *	
950 955	

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Ala	Pro	Tyr	Ser	Thr	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Glu	Thr	Pro
1				5					10					15

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